IFWO

RAW SEQUENCE LISTING DATE: 07/28/2004
PATENT APPLICATION: **US/09/545,998** TIME: 14:14:16

Input Set : **N:\Crf3\RULE60\09545998.raw**
Output Set: **N:\CRF4\07282004\I545998.raw**

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
5 (i) APPLICANT: Gorman, Daniel M.
6 Randall, Troy D.
7 Zlotnik, Albert
9 (ii) TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
10 REAGENTS
12 (iii) NUMBER OF SEQUENCES: 8
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: DNAX Research Institute
16 (B) STREET: 901 California Avenue
17 (C) CITY: Palo Alto
18 (D) STATE: California
19 (E) COUNTRY: USA
20 (F) ZIP: 94304-1104
22 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: Floppy disk
24 (B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
28 (vi) CURRENT APPLICATION DATA:
C--> 29 **(A) APPLICATION NUMBER: US/09/545,998**
C--> 30 **(B) FILING DATE: 10-Apr-2000**
W--> 35 **(C) CLASSIFICATION: 536**
C--> 40 **(vii) PRIOR APPLICATION DATA:**
33 (A) APPLICATION NUMBER: US/08/911,423
34 (B) FILING DATE: 14-AUG-1997
37 (A) APPLICATION NUMBER: US 60/023,419
38 (B) FILING DATE: 16-AUG-1996
41 (A) APPLICATION NUMBER: US 60/027,901
42 (B) FILING DATE: 07-OCT-1996
C--> 44 **(viii) ATTORNEY/AGENT INFORMATION:**
45 (A) NAME: Ching, Edwin P.
46 (B) REGISTRATION NUMBER: 34,090
47 (C) REFERENCE/DOCKET NUMBER: DX0612K
C--> 49 **(ix) TELECOMMUNICATION INFORMATION:**
50 (A) TELEPHONE: 650-852-9196
51 (B) TELEFAX: 650-496-1200
54 (2) INFORMATION FOR SEQ ID NO: 1:
56 (i) SEQUENCE CHARACTERISTICS:
57 (A) LENGTH: 1073 base pairs
58 (B) TYPE: nucleic acid
59 (C) STRANDEDNESS: single

ENTERED

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```
60           (D) TOPOLOGY: linear
62      (ii) MOLECULE TYPE: cDNA
65      (ix) FEATURE:
66           (A) NAME/KEY: CDS
67           (B) LOCATION: 68..751
70      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
72 CTCGAGATCC ATTGTGCTGG AAAGGGAACT CCTGAAATCA GCCGACAGAA GACTCAGGAG     60
74 AAGCACT ATG GGG GCA TGG GCC ATG CTG TAT GGA GTC TCG ATG CTC TGT      109
75         Met Gly Ala Trp Ala Met Leu Tyr Gly Val Ser Met Leu Cys
76           1               5                  10
78 GTG CTG GAC CTA GGT CAG CCG AGT GTA GTT GAG GAG CCT GGC TGT GGC      157
79 Val Leu Asp Leu Gly Gln Pro Ser Val Val Glu Glu Pro Gly Cys Gly
80  15                  20                  25                  30
82 CCT GGC AAG GTT CAG AAC GGA AGT GGC AAC AAC ACT CGC TGC TGC AGC      205
83 Pro Gly Lys Val Gln Asn Gly Ser Gly Asn Asn Thr Arg Cys Cys Ser
84                  35                  40                  45
86 CTG TAT GCT CCA GGC AAG GAG GAC TGT CCA AAA GAA AGG TGC ATA TGT      253
87 Leu Tyr Ala Pro Gly Lys Glu Asp Cys Pro Lys Glu Arg Cys Ile Cys
88               50                  55                  60
90 GTC ACA CCT GAG TAC CAC TGT GGA GAC CCT CAG TGC AAG ATC TGC AAG      301
91 Val Thr Pro Glu Tyr His Cys Gly Asp Pro Gln Cys Lys Ile Cys Lys
92           65                  70                  75
94 CAC TAC CCC TGC CAA CCA GGC CAG AGG GTG GAG TCT CAA GGG GAT ATT      349
95 His Tyr Pro Cys Gln Pro Gly Gln Arg Val Glu Ser Gln Gly Asp Ile
96       80                  85                  90
98 GTG TTT GGC TTC CGG TGT GTT GCC TGT GCC ATG GGC ACC TTC TCC GCA      397
99 Val Phe Gly Phe Arg Cys Val Ala Cys Ala Met Gly Thr Phe Ser Ala
100  95                  100                 105                 110
102 GGT CGT GAC GGT CAC TGC AGA CTT TGG ACC AAC TGT TCT CAG TTT GGA      445
103 Gly Arg Asp Gly His Cys Arg Leu Trp Thr Asn Cys Ser Gln Phe Gly
104                 115                 120                 125
106 TTT CTC ACC ATG TTC CCT GGG AAC AAG ACC CAC AAT GCT GTG TGC ATC      493
107 Phe Leu Thr Met Phe Pro Gly Asn Lys Thr His Asn Ala Val Cys Ile
108              130                 135                 140
110 CCG GAG CCA CTG CCC ACT GAG CAA TAC GGC CAT TTG ACT GTC ATC TTC      541
111 Pro Glu Pro Leu Pro Thr Glu Gln Tyr Gly His Leu Thr Val Ile Phe
112          145                 150                 155
114 CTG GTC ATG GCT GCA TGC ATT TTC TTC CTA ACC ACA GTC CAG CTC GGC      589
115 Leu Val Met Ala Ala Cys Ile Phe Phe Leu Thr Thr Val Gln Leu Gly
116      160                 165                 170
118 CTG CAC ATA TGG CAG CTG AGG AGG CAA CAC ATG TGT CCC CGA GAG ACC      637
119 Leu His Ile Trp Gln Leu Arg Arg Gln His Met Cys Pro Arg Glu Thr
120 175                 180                 185                 190
122 CAG CCA TTC GCG GAG GTG CAG TTG TCA GCT GAG GAT GCT TGC AGC TTC      685
123 Gln Pro Phe Ala Glu Val Gln Leu Ser Ala Glu Asp Ala Cys Ser Phe
124                 195                 200                 205
126 CAG TTC CCT GAG GAG GAA CGC GGG GAG CAG ACA GAA GAA AAG TGT CAT      733
127 Gln Phe Pro Glu Glu Glu Arg Gly Glu Gln Thr Glu Glu Lys Cys His
128              210                 215                 220
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CTG GGG GGT CGG TGG CCA TGAGGCCTGG TCTTCCTCTG TGCCCCAAGC 781
Leu Gly Gly Arg Trp Pro
225
CAGACGCTAC AAGACTTGCC CAGCTATACC CTTGGTGAGA GCAGGGGCCA TGCTCTGCAC 841
CCTTCCCTGG GCCTGGCCCT GCTCCCCTCA ACAGTGGCGG AAGTGGGTGT ATGAGAGCGG 901
TGAGTTACGA TTGGGCCCTA TGGCTGCCTT TCTCATTTGA CAGCTCTGTT GGAGTAGGGT 961
CTTTGGGCCC ACCAAGAGCA CCACGTTTAG CACAAGATCT TGTACAAGAA TAAATACTTG 1021
TTTAGTAACC TGAAAAAAAA AAAAAAAAGG GCGGCCGCGG AGGCCGAATT CC 1073

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Gly Ala Trp Ala Met Leu Tyr Gly Val Ser Met Leu Cys Val Leu
1 5 10 15
Asp Leu Gly Gln Pro Ser Val Val Glu Glu Pro Gly Cys Gly Pro Gly
20 25 30
Lys Val Gln Asn Gly Ser Gly Asn Asn Thr Arg Cys Cys Ser Leu Tyr
35 40 45
Ala Pro Gly Lys Glu Asp Cys Pro Lys Glu Arg Cys Ile Cys Val Thr
50 55 60
Pro Glu Tyr His Cys Gly Asp Pro Gln Cys Lys Ile Cys Lys His Tyr
65 70 75 80
Pro Cys Gln Pro Gly Gln Arg Val Glu Ser Gln Gly Asp Ile Val Phe
85 90 95
Gly Phe Arg Cys Val Ala Cys Ala Met Gly Thr Phe Ser Ala Gly Arg
100 105 110
Asp Gly His Cys Arg Leu Trp Thr Asn Cys Ser Gln Phe Gly Phe Leu
115 120 125
Thr Met Phe Pro Gly Asn Lys Thr His Asn Ala Val Cys Ile Pro Glu
130 135 140
Pro Leu Pro Thr Glu Gln Tyr Gly His Leu Thr Val Ile Phe Leu Val
145 150 155 160
Met Ala Ala Cys Ile Phe Phe Leu Thr Thr Val Gln Leu Gly Leu His
165 170 175
Ile Trp Gln Leu Arg Arg Gln His Met Cys Pro Arg Glu Thr Gln Pro
180 185 190
Phe Ala Glu Val Gln Leu Ser Ala Glu Asp Ala Cys Ser Phe Gln Phe
195 200 205
Pro Glu Glu Glu Arg Gly Glu Gln Thr Glu Glu Lys Cys His Leu Gly
210 215 220
Gly Arg Trp Pro
225

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1006 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..723
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```
ATG GCA CAG CAC GGG GCG ATG GGC GCG TTT CGG GCC CTG TGC GGC CTG        48
Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu
  1               5                  10                  15

GCG CTG CTG TGC GCG CTC AGC CTG GGT CAG CGC CCC ACC GGG GGT CCC        96
Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro
            20                  25                  30

GGG TGC GGC CCT GGG CGC CTC CTG CTT GGG ACG GGA ACG GAC GCG CGC       144
Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg
        35                  40                  45

TGC TGC CGG GTT CAC ACG ACG CGC TGC TGC CGC GAT TAC CCG GGC GAG       192
Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu
    50                  55                  60

GAG TGC TGT TCC GAG TGG GAC TGC ATG TGT GTC CAG CCT GAA TTC CAC       240
Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His
65                  70                  75                  80

TGC GGA GAC CCT TGC TGC ACG ACC TGC CGG CAC CAC CCT TGT CCC CCA       288
Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro
                85                  90                  95

GGC CAG GGG GTA CAG TCC CAG GGG AAA TTC AGT TTT GGC TTC CAG TGT       336
Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys
            100                 105                 110

ATC GAC TGT GCC TCG GGG ACC TTC TCC GGG GGC CAC GAA GGC CAC TGC       384
Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys
        115                 120                 125

AAA CCT TGG ACA GAC TGC ACC CAG TTC GGG TTT CTC ACT GTG TTC CCT       432
Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro
    130                 135                 140

GGG AAC AAG ACC CAC AAC GCT GTG TGC GTC CCA GGG TCC CCG CCG GCA       480
Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala
145                 150                 155                 160

GAG CCG CTT GGG TGG CTG ACC GTC GTC CTC CTG GCC GTG GCC GCC TGC       528
Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys
                165                 170                 175

GTC CTC CTC CTG ACC TCG GCC CAG CTT GGA CTG CAC ATC TGG CAG CTG       576
Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu
            180                 185                 190

AGG AGT CAG TGC ATG TGG CCC CGA GAG ACC CAG CTG CTG CTG GAG GTG       624
Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Leu Glu Val
        195                 200                 205

CCG CCG TCG ACC GAA GAC GCC AGA AGC TGC CAG TTC CCC GAG GAA GAG       672
Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu
    210                 215                 220
```

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```
275 CGG GGC GAG CGA TCG GCA GAG GAG AAG GGG CGG CTG GGA GAC CTG TGG       720
276 Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp
277 225                 230                 235                 240
279 GTG TGAGCCTGGC CGTCCTCCGG GGCCACCGAC CGCAGCCAGC CCCTCCCCAG            773
280 Val
283 GAGCTCCCCA GGCCGCAGGG GCTCTGCGTT CTGCTCTGGG CCGGGCCCTG CTCCCCTGGC     833
285 AGCAGAAGTG GGTGCAGGAA GGTGGCAGTG ACCAGCGCCC TGGACCATGC AGTTCGGCGG     893
287 CCGCTCTAAA GGATCCAAGC TTACGTACGC GTGCATGCGA CGTCATAGCT CTTCTATAGT     953
289 GTCACCTAAA TTCAATTCAC TGGCCGTCGT TTTACAACGT CCTGACTGGG AAA           1006
292 (2) INFORMATION FOR SEQ ID NO: 4:
294      (i) SEQUENCE CHARACTERISTICS:
295           (A) LENGTH: 241 amino acids
296           (B) TYPE: amino acid
297           (D) TOPOLOGY: linear
299      (ii) MOLECULE TYPE: protein
301      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
303 Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu
304   1               5                  10                  15
306 Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro
307              20                  25                  30
309 Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg
310          35                  40                  45
312 Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu
313      50                  55                  60
315 Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His
316  65                  70                  75                  80
318 Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro
319                  85                  90                  95
321 Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys
322             100                 105                 110
324 Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys
325         115                 120                 125
327 Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro
328     130                 135                 140
330 Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala
331 145                 150                 155                 160
333 Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys
334                 165                 170                 175
336 Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu
337             180                 185                 190
339 Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Leu Glu Val
340         195                 200                 205
342 Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu
343     210                 215                 220
345 Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp
346 225                 230                 235                 240
348 Val
351 (2) INFORMATION FOR SEQ ID NO: 5:
353      (i) SEQUENCE CHARACTERISTICS:
```

VERIFICATION SUMMARY DATE: 07/28/2004
PATENT APPLICATION: **US/09/545,998** TIME: 14:14:17

Input Set : **N:\Crf3\RULE60\09545998.raw**
Output Set: **N:\CRF4\07282004\I545998.raw**

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:35 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1)(vi)
L:36 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:40 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:44 M:220 C: Keyword misspelled or invalid format, [(viii) ATTORNEY/AGENT INFORMATION:]
L:49 M:220 C: Keyword misspelled or invalid format, [(ix) TELECOMMUNICATION INFORMATION:]